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Biotic interactions in the vineyard contribute to define grape productivity. Many microorganisms, including viruses, bacteria and fungi are capable of infecting grapevines causing important damage if left uncontrolled. Many more microorganisms, endophytic or epiphytic, are not pathogenic and may play a positive role in wine grape yield and chemical composition. Although recent reports have shown that composition of microbial communities correlates with quality characteristics and regional variation among wine grapes, our understanding of the interactions between microbial communities and grapevines is still limited. Here, I will discuss the use of whole genome sequencing based on single molecule real time sequencing (SMRT) technology to generate high-quality genome references for the plant host and the associated microorganisms to study their interactions under natural field settings. The highly heterozygous genome of Cabernet Sauvignon was sequenced at 140x coverage with the PacBio RSII using a combination of 20kb and 30kb DNA libraries. Reads were assembled into 788 contigs of total length of 590Mb, achieving a contig NG50 and NG90 of 2.1Mb and 1Mb, respectively. Genetic and optical maps are being used to improve contig scaffolding. The same approach was used to sequence the genomes of some of the most common and economically important fungal grape pathogens. For most species, SMRT sequencing yielded the reconstruction of entire chromosomes in individual contigs from telomore-to-telomere. These high quality genome sequences have provided us with the references necessary to apply metatranscriptomics and profile genome-wide gene expression of all interacting organisms simultaneously, including the grapevine host. Resequencing using short read technologies of multiple isolates and metatranscriptomic sequencing of vineyard samples has given us the opportunity to associate microbial activity, gene expression with genetic diversity. To study the impact of microbial activity on grape metabolism we have been integrating transcriptomics, metabolomics, and enzyme activity assays. Integrative systems-level analysis of grape berries during the interaction with biotrophic and necrotrophic pathogens is shading light on how microbial activities can reprogram berry development and metabolism.

1:15 pm

YOU SAY TOMATO, I SAY POTATO: HIGH-QUALITY GENOME ASSEMBLY OF THE SISTER-GROUP SPECIES *SOLANUM ETUBEROSUM* PROVIDES INSIGHTS INTO GENOME AND TRAIT EVOLUTION

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To elucidate the evolutionary history and basis of chromosomal, molecular and phenotypic differences between tomato and potato, genomic data from a key outgroup species is needed. *Solanum etuberosum*, a non-tuber-bearing species from Chile, fulfills this requirement: its ancestors diverged from the tomato-potato lineage shortly before the split of the tomato and potato clades. With the aim of investigating both genome and trait evolution, we sequenced and assembled the genome of *S. etuberosum*. The initial Illumina assembly consisted of 3666 scaffolds with the N50 statistic of 1.7Mb and captured 94% of the predicted 702 Mb genome size. The assembly was further scaffolded using BioNano genome mapping, yielding a final genome assembly that surpassed an N50 of 5Mb. Hence, it

is one of the most contiguous *Solanum* genome assemblies thus far, and with 97% coverage of the expected gene space, also one of the most complete ones. We subsequently annotated the genome sequence and reconstructed the evolution of genes crucial to potato and/or tomato phenotypes and specifically related to tuber formation, pathogen resistance, flower color and glycoalkaloid biosynthesis. The genome of *S. etuberosum* thus proved to be an invaluable resource for novel insights in the *Solanum* genus.

1:35 pm

UTILIZING LONG-RANGE SHORT-READ TECHNOLOGY FOR A BETTER PEPPER GENOME

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The pepper genome is one of the largest in Solanaceae at approximately 3.5 Gigabases and is comprised largely of repetitive elements estimated at 75-80% of the genome. As pepper is a diploid species, the genome structure has not inhibited production of multiple draft genome reference sequences using next generation sequencing technology with short reads. However, these genomes are largely comprised of a large number of small scaffolds with 37,989 scaffolds in the CM334, 967,017 scaffolds in the Zunla-1, and 1,973,483 scaffolds in the Chiltepin genomes with the largest scaffold N50 at 2.47Mb in the CM334 assembly. Recently third generation technologies have been released that capture long range sequence information in order to enhance the ability of generating higher quality reference sequences with a smaller number of larger scaffolds. These results have been promising on many different species in not only improving existing genomes, but generating new genomes de novo. Ability of breeders and researchers to use the pepper genome for improvement of the crop is dependent on a high-quality reference that provides anchoring and ordering of the majority of the sequence. Thus we have targeted the second generation 10X Genomics Chromium® technology for improving the pepper genome, by taking advantage of the long-range information together with affordable short-read technology. 10X Chromium not only builds on scaffolds, but allows for de novo genome assembly in a fraction of the time and cost with little input DNA. Importantly, the resulting assembly is phased as part of the assembly process, something that is not currently achievable using other technologies. Initial results indicate a significant improvement over any pepper short read genome assembly. We will report on the progress of generating a high quality pepper genome using this technology.

1:55 pm

NICOTIANA GENOMES: BEYOND TOBACCO

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While *Nicotiana tabacum* is likely the most notable species from the Nicotiana genus, various other Nicotiana species are cultivated as crops, grown as ornamental garden plants, or used as model organisms in research. Within Solanaceae, Nicotiana species are peculiar first because although most Solanaceae species are diploids, a high number of Nicotiana species are tetraploids; and second because they have relatively large genomes that are similar in size with Capsicum species and two to three times larger than Solanum and Petunia species.